STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/575,096_
Source: _Fwp_
Date Processed by STIC: _4/24/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/595,096_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
       Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 ____ Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES)   Sequence(s) ____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)   Sequence(s) ____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING   DATE: 04/24/2006
PATENT APPLICATION: US/10/575,096   TIME: 16:09:54

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

      3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
      5 <120> TITLE OF INVENTION: Process for the antibody composition using RNA
which inhibits a function
      6   of a1,6-fucosyltransferase
      8 <130> FILE REFERENCE: 11621WO1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/575,096
C--> 10 <141> CURRENT FILING DATE: 2006-04-10
     10 <150> PRIOR APPLICATION NUMBER: P2003-350167
     11 <151> PRIOR FILING DATE: 2003-10-09
E--> 13 <160> NUMBER OF SEQ ID NOS: 35
     15 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

    266 <210> SEQ ID NO: 5
    267 <211> LENGTH: 575
    268 <212> TYPE: PRT
    269 <213> ORGANISM: Cricetulus griseus
    271 <400> SEQUENCE: 5
    272 Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
    273   1   5   10   15
    275 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
    276   20   25   30
    278 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
    279   35   40   45
    281 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
    282   50   55   60
    284 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
    285 65   70   75   80
    287 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
    288   85   90   95
    290 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Asp Leu Gly Lys Asp His
    291   100   105   110
    293 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
    294   115   120   125
    296 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Lys Leu Glu Gly Asn Glu
    297   130   135   140
    299 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
    300 145   150   155   160
    302 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
    303   165   170   175
    305 Gly Glu Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
    306   180   185   190

RAW SEQUENCE LISTING   DATE: 04/24/2006
PATENT APPLICATION: US/10/575,096   TIME: 16:09:54

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

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308 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
309         195                 200                 205
311 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
312         210                 215                 220
314 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
315 225                 230                 235                 240
317 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
318         245                 250                 255
320 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
321         260                 265                 270
323 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
324         275                 280                 285
326 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
327         290                 295                 300
329 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
330 305                 310                 315                 320
332 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
333         325                 330                 335
335 Arg Pro Gln Pro Trp Leu Glu Arg Glu Ile Glu Glu Thr Thr Lys Lys
336         340                 345                 350
338 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
339         355                 360                 365
341 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
342         370                 375                 380
344 His Val Glu Glu His Phe Gln Leu Leu Glu Arg Arg Met Lys Val Asp
345 385                 390                 395                 400
347 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
348         405                 410                 415
350 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
351         420                 425                 430
353 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
354         435                 440                 445
356 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
357         450                 455                 460
359 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
360 465                 470                 475                 480
362 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
363         485                 490                 495
365 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
366         500                 505                 510
368 His Gln Pro Arg Thr Lys Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
369         515                 520                 525
371 Ile Gly Val Ala Gly Asn His Trp Asn Gly Tyr Ser Lys Gly Val Asn
372         530                 535                 540
374 Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
375 545                 550                 555                 560
377 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
378                 565                 570
381 <210> SEQ ID NO: 6
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E--> 378

575 insert

P.4

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/575,096

DATE: 04/24/2006
TIME: 16:09:54

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

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383 <212> TYPE: PRT
384 <213> ORGANISM: Mus musculus
386 <400> SEQUENCE: 6
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390 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
391                 20                  25                  30
393 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
394                 35                  40                  45
396 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
397         50                  55                  60
399 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
400  65                  70                  75                  80
402 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
403                 85                  90                  95
405 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
406                 100                 105                 110
408 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
409             115                 120                 125
411 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
412         130                 135                 140
414 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
415 145                 150                 155                 160
417 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
418                 165                 170                 175
420 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
421             180                 185                 190
423 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
424         195                 200                 205
426 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
427         210                 215                 220
429 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
430 225                 230                 235                 240
432 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
433                 245                 250                 255
435 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
436                 260                 265                 270
438 Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
439         275                 280                 285
441 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
442         290                 295                 300
444 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Leu Arg Val His
445 305                 310                 315                 320
447 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
448                 325                 330                 335
450 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
451                 340                 345                 350
453 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
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RAW SEQUENCE LISTING   DATE: 04/24/2006
PATENT APPLICATION: US/10/575,096   TIME: 16:09:54

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

```
454         355               360               365
456 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
457     370               375               380
459 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
460 385               390               395               400
462 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Thr Leu Leu Lys Glu
463               405               410               415
465 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
466               420               425               430
468 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
469               435               440               445
471 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
472     450               455               460
474 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
475 465               470               475               480
477 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
478               485               490               495
480 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
481               500               505               510
483 His Lys Pro Arg Thr Glu Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
484               515               520               525
486 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn
487     530               535               540
489 Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
490 545               550               555               560
492 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
493               565               570
```

replace with E--> 493
⟨213⟩

```
496 <210> SEQ ID NO: 7
497 <211> LENGTH: 575
498 <212> TYPE: PRT
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E--> 499 ⟨214⟩ Rattus norvegicus   *see p. 6*

⟨214⟩ *is invalid*

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501 <400> SEQUENCE: 7
502 Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
503 1               5               10              15
505 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
506               20              25              30
508 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
509               35              40              45
511 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
512     50              55              60
514 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr
515 65              70              75              80
517 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
518               85              90              95
520 Ile Glu Asn Tyr Lys Lys Gln Ala Arg Asn Gly Leu Gly Lys Asp His
521               100             105             110
523 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
524               115             120             125
```

```
526 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys His Leu Glu Gly Asn Glu
527     130                 135                 140
529 Leu Gln Arg His Ala Asp Glu Ile Leu Leu Asp Leu Gly His His Glu
530 145                 150                 155                 160
532 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
533                 165                 170                 175
535 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
536                 180                 185                 190
538 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Arg
539                 195                 200                 205
541 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
542     210                 215                 220
544 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
545 225                 230                 235                 240
547 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
548                 245                 250                 255
550 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu
551                 260                 265                 270
553 Ser Thr Gly His Trp Ser Gly Glu Val Asn Asp Lys Asn Ile Gln Val
554             275                 280                 285
556 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
557     290                 295                 300
559 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
560 305                 310                 315                 320
562 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
563                 325                 330                 335
565 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
566             340                 345                 350
568 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
569         355                 360                 365
571 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
572     370                 375                 380
574 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
575 385                 390                 395                 400
577 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
578                 405                 410                 415
580 Ala Lys Thr Lys Tyr Ser Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
581             420                 425                 430
583 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
584             435                 440                 445
586 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
587     450                 455                 460
589 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
590 465                 470                 475                 480
592 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
593                 485                 490                 495
595 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
596             500                 505                 510
598 His Lys Pro Arg Thr Asp Glu Glu Ile Pro Met Glu Pro Gly Asp Ile
```

```
599          515                   520                   525
601 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn
602     530                   535        .           540
604 Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
605 545               550                   555               560
607 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys                575 ← insert
E--> 608               565                   570
611 <210> SEQ ID NO: 8
⟨2137 612 <211> LENGTH: 575                                    → same error
613 <212> TYPE: PRT                                        in sequence 4
E--> 614 <215> Homo Sapience  Sapiens
616                                                see p.7
616 <400> SEQUENCE: 8
617 Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
618   1               5                   10                  15
620 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
621               20                  25                  30
623 Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
624           35                  40                  45              .
626 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
627       50                  55                  60
629 Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ile
630   65                  70                  75                  80
632 Gly Arg Val Arg Val Leu Glu Glu Gln Leu Val Lys Ala Lys Glu Gln
633               85                  90                  95
635 Ile Glu Asn Tyr Lys Lys Gln Thr Arg Asn Gly Leu Gly Lys Asp His
636           100                 105                 110
638 Glu Ile Leu Arg Arg Arg Ile Glu Asn Gly Ala Lys Glu Leu Trp Phe
639           115                 120                 125
641 Phe Leu Gln Ser Glu Leu Lys Lys Leu Lys Asn Leu Glu Gly Asn Glu
642       130                 135                 140
644 Leu Gln Arg His Ala Asp Glu Phe Leu Leu Asp Leu Gly His His Glu
645 145               150                 155                 160
647 Arg Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala
648           165                 170                 175
650 Gly Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln
651           180                 185                 190
653 Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys
654           195                 200                 205
656 Lys Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu
657       210                 215                 220
659 His His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr
660 225               230                 235                 240
662 Leu Ile Leu Glu Ser Gln Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu
664           245                 250                 255
666 Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ile
667           260                 265                 270
669 Ser Thr Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val
670           275                 280                 285
```

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\04242006\J575096.raw

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672 Val Glu Leu Pro Ile Val Asp Ser Leu His Pro Arg Pro Pro Tyr Leu
673     290             295             300
675 Pro Leu Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His
676 305             310             315             320
678 Gly Asp Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile
679             325             330             335
681 Arg Pro Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys
682             340             345             350
684 Leu Gly Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp
685             355             360             365
687 Lys Val Gly Thr Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Met Val
688     370             375             380
690 His Val Glu Glu His Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp
691 385             390             395             400
693 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ser Leu Leu Lys Glu
694             405             410             415
696 Ala Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile
697             420             425             430
699 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
700             435             440             445
702 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
703     450             455             460
705 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
706 465             470             475             480
708 Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
709             485             490             495
711 Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala
712             500             505             510
714 His Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile
715             515             520             525
717 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn
718     530             535             540
720 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
721 545             550             555             560
723 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
E--> 724             565             570
```

<400> 50
gaa ttc ggc atc atg tgg cag ctg ctc ctc cca act gct ctg cta ctt   48
            Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu
            1   ±   `   5   -5   `   10 -10-

misaligned numbers

<400> 53
gaa ttc ggc atc atg tgg cag ctg ctc ctc cca act gct ctg cta ctt   48
              Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu
              1   1   5   5   10 10

resequenced numbers

<210> 54
<211> 199   *last sequence in file*
<212> PRT
<213> Homo sapiens

<400> 54

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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
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            20                  25                  30
Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
            35                  40                  45
Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
    50                  55                  60
Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65                  70                  75                  80
Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
                85                  90                  95
Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
            100                 105                 110
Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
            115                 120                 125
His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
    130                 135                 140
Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145                 150                 155                 160
Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
            165                 170                 175
Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
            180                 185                 190
Gly His His His His His His
            195
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1/38 *delete*

11

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\04242006\J575096.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:378 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:493 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:499 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:501 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:608 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:614 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER
L:616 M:282 E: Numeric Field Identifier Missing, <213> is required.
L:724 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:1044 M:283 W: Missing Blank Line separator, <220> field identifier
L:1045 M:283 W: Missing Blank Line separator, <400> field identifier
L:1114 M:283 W: Missing Blank Line separator, <220> field identifier
L:1241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1277 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1361 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1373 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1376 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:1388 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:53
L:13 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (35) Counted
(54)